AMENDMENTS TO THE SPECIFICATION

Please replace paragraph 0023 with the following rewritten paragraph:

[0023] FIG. 2 shows the design of the primers, probes, and capture sequences of the CYP2D6 SNP Assay method (~~SEQ ID NOS: 17-22, 5-6, 23-24, 7-8 and 25-26~~ SEQ ID. NOs. 1, 2, 17, 18, 3, 4, 21, 22, 5, 6, 23, 24, 7, 8, 25, and 26, respectively, in order of appearance).

Please replace paragraph 0024 with the following rewritten paragraph:

[0024] FIG. 3 schematically illustrates the primers and probes used to detect an SNP in multiplex mode, and using [[Luminex™]] LUMINEX® microspheres.

Please replace paragraph 0034 with the following rewritten paragraph:

[0034] As used herein, the term "probe" refers to a structure comprised of a polynucleotide that forms a hybrid structure with a target sequence contained in a molecule (a "target molecule") in a sample undergoing analysis, due to complementarity of at least one sequence in the probe with the target sequence. The nucleotides of any particular probe may be deoxyribonucleotides, ribonucleotides, and/or synthetic nucleotide analogs. The term "primer" refers to a molecule that comprises an oligonucleotide, whether produced naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product that is complementary to a nucleic acid strand is induced, i.e., in the presence of appropriate nucleotides and an agent for polymerization such as a DNA polymerase in an appropriate buffer and at a suitable temperature. Preferred primers for use herein are the dual-purpose primers described in U.S. Patent Application No. 10/667,191 to Quinn et al. for "Dual-Purpose Primers and Probes for Providing Enhanced Hybridization Assays by Disruption of Secondary Structure Formation," filed on even date herewith.

Please replace paragraph 0064 with the following rewritten paragraph:

[0064] Optimally, a flow cytometer linked with one or more detecting means is used for detecting the complexes, although other means for detecting and counting the captured complexes can also be used, depending on the type of label and signal. The complexes in the hybridization solution are passed through the flow cytometer, thereby allowing the detection of each complex. Preferably, the flow

cytometer is linked with a first detecting means for detecting the label (of the labeled amplicon) as well as a second detecting means for detecting the signal associated with the solid substrate. Suitable equipment and methods for detecting the labels and signals using flow cytometry, and having the ability to perform multiplexing analysis, are described in U.S. Patent Nos. 5,981,180 to Chandler et al., and 6,046,807 and 6,139,800 to Chandler. Commercially available systems are also available from Luminex Corp. (Austin, Texas) and include, for example, the [[Luminex™]] LUMINEX® 100 machine.

Please amend paragraph 0082 with the following rewritten paragraph:

[0082] To carryout the procedures set forth below, a variety of software was used for primer design and Tm prediction, including Primer3, [[GCG®]] GCC®, VNTI, [[Primer Express®]] PRIMER EXPRESS®, and Hybsimulator. Hybsimulator was found to be the preferred software for Tm prediction.

Please amend the heading for the example on page 19 of the application, immediately below paragraph 0082 and above paragraph 0083 with the following amended heading:

EXAMPLE

DETECTION OF WILD TYPE OR MUTANT ALLELES FOR EXONS 1, 2, 6, AND 9 OF CYTOCHROME P450 ~~CPY2D6~~ CYP2D6

Please amend paragraph 0083 with the following rewritten paragraph:

[0083] As the first step in the detection of wild-type and mutant alleles for exons 1, 2, 6, and 9 of cytochrome P450 ~~CPY2D6~~ CYP2D6, the following forward and reverse primers were prepared:

Primer		Primer Sequence	Sequence ID No.	Primer Length
Exon 1	forward:	biotin-tagtggccatcttcctgctc	(SEQ ID NO: 1)	20
	reverse:	tctggtaggggagcctcag	(SEQ ID NO: 2)	19
Exon 2	forward:	biotin-cttcggggacgtgttcag	(SEQ ID NO: 3)	18
	reverse:	tcccacggaaatctgtctct	(SEQ ID NO: 4)	20
Exon 6	forward:	biotin-cccgttctgtcccgagtat	(SEQ ID NO: 5)	19
	reverse:	gtttcccagatgggctcac	(SEQ ID NO: 6)	19
Exon 9	forward:	biotin-ccatggtgtctttgctttcc	(SEQ ID NO: 7)	20
	reverse:	gtggggtaagcaggaatgag	(SEQ ID NO: 8)	20

Please replace paragraph 0084 with the following rewritten paragraph:

[0084] As the second step in the detection of wild-type and mutant alleles for exons 1, 2, 6, and 9 of cytochrome P450 ~~CPY2D6~~ CYP2D6, human genomic DNA was extracted from 200 µL of EDTA-treated whole blood using [[QIAamp®]] QIAMP® DNA Blood Mini Kit as described by the manufacturer (Qiagen).

Please replace paragraph 0085 with the following rewritten paragraph:

[0085] As the third step in the detection of wild type or mutant alleles for exons 1, 2, 6, and 9 of cytochrome P450 ~~CPY2D6~~ CYP2D6, allele specific hybridization probes were designed for use in a multiplexing mode. The presence or absence of a SNP in each of exons 1, 2, 6, and 9 was determined using allele specific hybridization probes comprising a sequence complementary to either the wild type or mutant allele, and further comprising unique capture sequences that are complementary to sequences attached to [[Luminex™]] LUMINEX® beads having unique color codes; the color detected indicating the identity of the allele specific sequence, and thus the presence of the wild type or mutant sequence in the target nucleotide sequence. The capture sequences were designed to minimize the potential non-specific binding to genomic DNA sequences that may be present in the amplified sequences by incorporating iso-cytosine and iso-guanine into the capture probes and complementary sequences attached to the Luminex[[™]]® beads.

Please replace paragraph 0087 with the following rewritten paragraph:

[0087] The fourth step in the detection of wild type or mutant alleles for exons 1, 2, 6, and 9 of cytochrome P450 ~~CPY2D6~~ CPY2D6, is the carrying out of a singleplex or multiplex polymerase chain reaction. In the present example, the singleplex or multiplex PCR was carried out using 2 µL (50-70 ng) isolated genomic DNA. Twenty-five microliter reaction volumes were prepared containing 1x Titanium Taq PCR buffer; 2.5 mM each dNTP's (dATP, dCTP, dGTP, and dTTP); 0.2µM each forward (biotinylated) and reverse primers; and 2.5 U Titanium Taq DNA polymerase. A PE 9600 thermocycler was used. The thermal cycling conditions were 94°C for 2 min followed by 30 cycles of 95°C for 30 sec, 68°C for 1 minute, followed by a final extension of 5 min at 68°C.

Please replace paragraph 0088 with the following rewritten paragraph:

The final step in the detection of wild type or mutant alleles for exons 1, 2, 6, and 9 of cytochrome P450 ~~CPY2D6~~ CPY2D6, is the SNP Assay, shown in FIG. 1 and carried out as follows. After the PCR reaction was complete, 25 µL of multiplex working reagent was added to the individual wells containing the multiplex PCR products. The plate was sealed with mylar and the incubation was continued in the PE 9600 thermocycler. The multiplex working reagent contained 0.1 pmol each allele specific hybridization probe (ASH) for the four SNP regions and 2000 each individual [[Luminex™]] LUMINEX® microspheres per 25 µL of 50 mM Hepes containing 500 mM LiCl, 1 % LDS, 1% BSA, 10 mM $MgCl_2$, 0.01 mM $ZnCl_2$ and 0.5% sodium azide and Proclin-300 as a preservative (HIV 3.0 Label Diluent, Bayer Diagnostics), having a final pH of 7.5. The PCR plate with the multiplex ASH working reagent was incubated for 10 minutes at 95°C to dissociate double stranded DNA followed by a 30 minute incubation at 50°C to achieve allele specific hybridization. The plate was removed and 100 µL of wash buffer was added to each well (HIV 3.0 Wash A, Bayer Diagnostics). The contents of the wells were transferred to a 96 well pre-wetted filter plate ([[MultiScreen®-BV]] MULTISCREEN-BV® 1.2 µm, Millipore, Bedford MA). The wash buffer was pulled through with gentle vacuum and a 200 µL wash was repeated. The microspheres were resuspended in a 50 µL streptavidin-phycoerythrin, (0.05µg/50µL) TTL buffer (50 mM Tris, 400 mM LiCl, 0.1% Tween-20, pH 8.0) mixture. The plate was then wrapped in aluminum foil and incubated for 15 minutes at 25°C with mild shaking (Titer Plate shaker, Labline Instruments). The previous wash step was repeated and the microspheres were resuspended in 80 µL of TTL buffer and read on the [[Luminex™]] LUMINEX® 100 in which the presence of phycoerythrin (and hence the original forward primer) and the microspheres specific for each particular ASH were detected. FIG. 2 shows the capture region for the wild type and variant discrimination probes for each of exons 1, 2, 6, and 9 of the cytochrome P450 ~~CPY2D6~~ CYP2D6 gene; FIG. 3 shows how the SNP assay results in the different color [[Luminex™]] LUMINEX® 100 beads; and FIG. 4 shows the results of the SNP P450 Assay for four individual patients.